

1600



OIPE

## RAW SEQUENCE LISTING

DATE: 07/15/2003

PATENT APPLICATION: US/09/663,481

TIME: 10:59:30

Input Set : A:\PC10350AGPR.ST25.txt

Output Set: N:\CRF4\07152003\I663481.raw

RECEIVED  
AUG 2 5 2003  
TECH CENTER 1600/2900

3 <110> APPLICANT: Pfizer Inc.  
4       Fidock, Mark D.  
6 <120> TITLE OF INVENTION: PHOSPHODIESTERASE ENZYMES  
8 <130> FILE REFERENCE: PC10350AGPR  
10 <140> CURRENT APPLICATION NUMBER: US 09/663,481  
11 <141> CURRENT FILING DATE: 2000-09-15  
13 <150> PRIOR APPLICATION NUMBER: US 60/177,326  
14 <151> PRIOR FILING DATE: 2000-01-20  
16 <150> PRIOR APPLICATION NUMBER: UK 9922125.1  
17 <151> PRIOR FILING DATE: 1999-09-17  
19 <160> NUMBER OF SEQ ID NOS: 21  
21 <170> SOFTWARE: PatentIn version 3.2  
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38 Ile Glu Glu Leu Lys Lys Asn Leu Glu Tyr Thr Ala Ser Leu Leu Glu  
39                       35                       40                       45  
42 Ala Val Tyr Ile Asp Glu Thr Arg Gln Ile Leu Asp Thr Glu Asp Glu  
43                       50                       55                       60  
46 Leu Gln Glu Leu Arg Ser Asp Ala Val Pro Ser Glu Val Arg Asp Trp  
47 65                       70                       75                       80  
50 Leu Ala Ser Thr Phe Thr Gln Gln Ala Arg Ala Lys Gly Arg Arg Ala  
51                       85                       90                       95  
54 Glu Glu Lys Pro Lys Phe Arg Ser Ile Val His Ala Val Gln Ala Gly  
55                       100                       105                       110  
58 Ile Phe Val Glu Arg Met Phe Arg Arg Thr Tyr Thr Ser Val Gly Pro  
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62 Thr Tyr Ser Thr Ala Val Leu Asn Cys Leu Lys Asn Leu Asp Leu Trp  
63                       130                       135                       140  
66 Cys Phe Asp Val Phe Ser Leu Asn Gln Ala Ala Asp Asp His Ala Leu  
67 145                       150                       155                       160  
70 Arg Thr Ile Val Phe Glu Leu Leu Thr Arg His Asn Leu Ile Ser Arg  
71                       165                       170                       175  
74 Phe Lys Ile Pro Thr Val Phe Leu Met Ser Phe Leu Asp Ala Leu Glu  
75                       180                       185                       190  
78 Thr Gly Tyr Gly Lys Tyr Lys Asn Pro Tyr His Asn Gln Ile His Ala  
79                       195                       200                       205

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87 225      230      235      240
90 Ala Ile His Asp Tyr Glu His Thr Gly Thr Asn Ser Phe His Ile
91      245      250      255
94 Gln Thr Lys Ser Glu Cys Ala Ile Val Tyr Asn Asp Arg Ser Val Leu
95      260      265      270
98 Glu Asn His His Ile Ser Ser Val Phe Arg Leu Met Gln Asp Asp Glu
99      275      280      285
102 Met Asn Ile Phe Ile Asn Leu Thr Lys Asp Glu Phe Val Glu Leu Arg
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106 Ala Leu Val Ile Glu Met Val Leu Ala Thr Asp Met Ser Cys His Phe
107 305      310      315      320
110 Gln Gln Val Lys Thr Met Lys Thr Ala Leu Gln Gln Leu Glu Arg Ile
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114 Asp Lys Pro Lys Ala Leu Ser Leu Leu Leu His Ala Ala Asp Ile Ser
115      340      345      350
118 His Pro Thr Lys Gln Trp Leu Val His Ser Arg Trp Thr Lys Ala Leu
119      355      360      365
122 Met Glu Glu Phe Phe Arg Gln Gly Asp Lys Glu Ala Glu Leu Gly Leu
123      370      375      380
126 Pro Phe Ser Pro Leu Cys Asp Arg Thr Ser Thr Leu Val Ala Gln Ser
127 385      390      395      400
130 Gln Ile Gly Phe Ile Asp Phe Ile Val Glu Pro Thr Phe Ser Val Leu
131      405      410      415
134 Thr Asp Val Ala Glu Lys Ser Val Gln Pro Leu Ala Asp Glu Asp Ser
135      420      425      430
138 Lys Ser Lys Asn Gln Pro Ser Phe Gln Trp Arg Gln Pro Ser Leu Asp
139      435      440      445
142 Val Glu Val Gly Asp Pro Asn Pro Asp Val Val Ser Phe Arg Ser Thr
143      450      455      460
146 Trp Val Lys Arg Ile Gln Glu Asn Lys Gln Lys Trp Lys Glu Arg Ala
147 465      470      475      480
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172 catggcaaac cctgttcttg tttagaggag ccacctccag ggccccattc tcaggctgcg      180
174 ctacatggtg aagcagtttg agaatgggga gataaacatt gaggagctga agaaaaatct      240

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180	gctggcctcc	accttcaccc	agcaggcccc	ggccaaaggc	cgccgagcag	aggagaagcc	420
182	caagttccga	agcattgtgc	acgctgtgca	ggctgggac	ttcgtggaac	ggatgttccg	480
184	gagaacatac	acctctgttg	gccccactta	ctctactgcg	gttctcaact	gtctcaagaa	540
186	cctggatctc	tggtgctttg	atgtcttttc	cttgaaccag	gcagcagatg	accatgccct	600
188	gaggaccatt	gtttttgagt	tgctgactcg	gcataacctc	atcagccgct	tcaagattcc	660
190	cactgtgttt	ttgatgagtt	tcctggatgc	cttggagaca	ggctatggga	agtacaagaa	720
192	tccttaccac	aaccagatcc	acgcagccga	tgttaccacg	acagtccatt	gcttcttgct	780
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196	agctatccat	gattatgagc	acacgggcac	taccaacagc	ttccacatcc	agaccaagtc	900
198	agaatgtgcc	atcgtgtaca	atgatcgttc	agtgtctggg	aatcaccaca	tcagctctgt	960
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202	tgtagaactc	cgagccctgg	tcattgagat	gggtgttgcc	acagacatgt	cctgccattt	1080
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275 <212> TYPE: PRT
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278 <400> SEQUENCE: 3
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289 35 40 45
292 Gly Glu Ile Asn Ile Glu Glu Leu Lys Lys Asn Leu Glu Tyr Thr Ala
293 50 55 60
296 Ser Leu Leu Glu Ala Val Tyr Ile Asp Glu Thr Arg Gln Ile Leu Asp
297 65 70 75 80
300 Thr Glu Asp Glu Leu Gln Glu Leu Arg Ser Asp Ala Val Pro Ser Glu
301 85 90 95
304 Val Arg Asp Trp Leu Ala Ser Thr Phe Thr Gln Gln Ala Arg Ala Lys
305 100 105 110
308 Gly Arg Arg Ala Glu Glu Lys Pro Lys Phe Arg Ser Ile Val His Ala
309 115 120 125
312 Val Gln Ala Gly Ile Phe Val Glu Arg Met Phe Arg Arg Thr Tyr Thr
313 130 135 140
316 Ser Val Gly Pro Thr Tyr Ser Thr Ala Val Leu Asn Cys Leu Lys Asn
317 145 150 155 160
320 Leu Asp Leu Trp Cys Phe Asp Val Phe Ser Leu Asn Gln Ala Ala Asp
321 165 170 175
324 Asp His Ala Leu Arg Thr Ile Val Phe Glu Leu Leu Thr Arg His Asn
325 180 185 190
328 Leu Ile Ser Arg Phe Lys Ile Pro Thr Val Phe Leu Met Ser Phe Leu
329 195 200 205
332 Asp Ala Leu Glu Thr Gly Tyr Gly Lys Tyr Lys Asn Pro Tyr His Asn
333 210 215 220
336 Gln Ile His Ala Ala Asp Val Thr Gln Thr Val His Cys Phe Leu Leu
337 225 230 235 240
340 Arg Thr Gly Met Val His Cys Leu Ser Glu Ile Glu Leu Leu Ala Ile
341 245 250 255
344 Ile Phe Ala Ala Ala Ile His Asp Tyr Glu His Thr Gly Thr Thr Asn
345 260 265 270
348 Ser Phe His Ile Gln Thr Lys Ser Glu Cys Ala Ile Val Tyr Asn Asp
349 275 280 285
352 Arg Ser Val Leu Glu Asn His Ile Ser Ser Val Phe Arg Leu Met
353 290 295 300
356 Gln Asp Asp Glu Met Asn Ile Phe Ile Asn Leu Thr Lys Asp Glu Phe
357 305 310 315 320
360 Val Glu Leu Arg Ala Leu Val Ile Glu Met Val Leu Ala Thr Asp Met
361 325 330 335
364 Ser Cys His Phe Gln Gln Val Lys Thr Met Lys Thr Ala Leu Gln Gln
365 340 345 350
368 Leu Glu Arg Ile Asp Lys Pro Lys Ala Leu Ser Leu Leu Leu His Ala

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369          355          360          365
372 Ala Asp Ile Ser His Pro Thr Lys Gln Trp Leu Val His Ser Arg Trp
373          370          375          380
376 Thr Lys Ala Leu Met Glu Phe Phe Arg Gln Gly Asp Lys Glu Ala
377 385          390          395          400
380 Glu Leu Gly Leu Pro Phe Ser Pro Leu Cys Asp Arg Thr Ser Thr Leu
381          405          410          415
384 Val Ala Gln Ser Gln Ile Gly Phe Ile Asp Phe Ile Val Glu Pro Thr
385          420          425          430
388 Phe Ser Val Leu Thr Asp Val Ala Glu Lys Ser Val Gln Pro Leu Ala
389          435          440          445
392 Asp Glu Asp Ser Lys Ser Lys Asn Gln Pro Ser Phe Gln Trp Arg Gln
393          450          455          460
396 Pro Ser Leu Asp Val Glu Val Gly Asp Pro Asn Pro Asp Val Val Ser
397 465          470          475          480
400 Phe Arg Ser Thr Trp Val Lys Arg Ile Gln Glu Asn Lys Gln Lys Trp
401          485          490          495
404 Lys Glu Arg Ala Ala Ser Gly Ile Thr Asn Gln Met Ser Ile Asp Glu
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412 His Asn Gln Asn Gly Asn Leu Asp
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419 <213> ORGANISM: Homo sapiens
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426 ggagtcggat tgcccgtcac ccctggagct gaagtcagcc ccagcaaga agatgtggat      180
428 taagcttcgg tctctgctgc gctacatggt gaagcagttg gagaatgggg agataaacat      240
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434 gccttcggag gtgcgggact ggctggcctc caccttcacc cagcaggccc gggccaaagg      420
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442 ggcagcagat gaccatgccc tgaggacatc tgtttttgag ttgctgactc ggcataacct      660
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RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/09/663,481

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Input Set : A:\PC10350AGPR.ST25.txt  
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,  
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:14,15,16,17,18,19,20,21

**VERIFICATION SUMMARY**

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Input Set : A:\PC10350AGPR.ST25.txt

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